

Application No. Not yet known

Page 1, line 9, after "filed April 10, 1995," please insert ~~now U.S. Patent No.~~

Q2 5,591,573, issued January 7, 1997, --.

In the Claims:

Please delete claims 1-8.

Please add the following new claims 9-27:

-- 9. A method for uniquely identifying viral positive biological fluid donations in the fewest number of PCR analysis cycles, the method comprising:
 providing a multiplicity of biological fluid donations;
 defining an n-dimensional matrix, where n is an integer, the matrix further comprising a multiplicity of internal elements, each element defined by an intersection of the n-dimensions of the matrix, each individual element identified by a respective matrix notation, the matrix notation comprising at least an index for each dimension of the array;
 taking a sample from each of the multiplicity of biological fluid donations;
 mapping each sample to a respective particular one of each element of the matrix, each individual sample identified by its corresponding element's respective matrix notation;
 taking aliquots from each sample, the number of aliquots taken from each sample defined by the number of dimensions characterizing the matrix;
 forming subpools from the aliquots of each sample, each subpool containing an aliquot from all samples identified by a matrix notation in which one dimensional index is fixed, each respective subpool identified by said fixed dimensional index;

Application No. Not yet known

19 providing the subpools to a PCR testing facility, wherein all of the
20 subpools are tested for viral indication in a single PCR analysis cycle;

21 determining the respective fixed dimensional indices of subpools which
22 return a positive viral indication; and

23 combining said fixed dimensional indices into a matrix notation, thereby
24 unambiguously identifying a unique matrix element defined by the matrix notation,
25 thus unambiguously identifying a uniquely viral positive sample. --

1 -- 10. ² The method according to claim ⁹, wherein the matrix is constructed as a
2 regular array, each of the array's n-dimensions characterized by an equal, integer
3 number of elements. --

1 -- 11. ³ The method according to claim ¹⁰, ² wherein the regular array comprises
2 a 3-dimensional array, the array further subdivided into rows, columns, and layers,
3 and wherein each element is characterized by a matrix notation X_{rcs} , where the
4 dimensional indices r, c, and s, respectively, identify elements comprising a row, a
5 column, and a layer of the array. --

1 -- 12. The method according to claim 11, ¹ wherein the subpool formation step
2 further comprises:

3 forming subpools of aliquots from samples identified by identical r indices
4 but different c and s indices;

5 forming subpools of aliquots from samples identified by identical c indices
6 but different r and s indices;

7 forming subpools of aliquots from samples identified by identical s indices
8 but different r and c indices; and

9 evaluating each of the r, c, and s subpools for a viral positive indication
10 returned by PCR testing. --

Application No. Not yet known

1 -- ⁵ 18. The method according to claim ⁴ 12 further comprising the steps of:
2 determining the integer index of each r subpool which returned a positive
3 viral indication;
4 determining the integer index of each c subpool which returned a positive
5 viral indication; and
6 determining the integer index of each s subpool which returned a positive
7 viral indication. --

1 -- ⁶ 14. The method according to claim ⁵ 13 further comprising the step of
2 substituting the integer indices of each r, c, and s subpool which returned a positive
3 viral indication for the dimensional indices r, c, and s of the matrix notation, thereby
4 identifying a unique matrix element defined by said matrix notation, thus uniquely
5 identifying the corresponding viral positive sample. --

1 -- ⁷ 15. The method according to claim ⁶ 14, wherein the 3-dimensional array
2 comprises an $8 \times 8 \times 8$ regular array, the dimensional indices r, c, and s each taking on
3 integer values from 1 to 8. --

1 -- ⁸ 16. The method according to claim ⁷ 15, wherein three aliquots are taken from
2 each respective sample of the biological fluid donations. --

1 -- ⁹ 17. The method according to claim ⁸ 16, further comprising the steps of:
2 forming eight row subpools, each row subpool uniquely identified by an
3 integer from 1 to 8, each row subpool formed from 64 sample aliquots;
4 forming eight column subpools, each column subpool uniquely identified
5 by an integer from 1 to 8, each column subpool formed from 64 sample aliquots; and

Application No. Not yet known

6 forming eight layer subpools, each layer subpool uniquely identified by an
7 integer from 1 to 8, each layer subpool formed from 64 sample aliquots. --

1 -- 18. A method for uniquely identifying viral positive biological fluid donations
2 in the fewest number of PCR analysis cycles, the method comprising:

3 providing a multiplicity of biological fluid donations;

4 defining an n-dimensional matrix, where n is an integer, the matrix
5 further comprising a multiplicity of internal elements, each element defined by an
6 intersection of the n-dimensions of the matrix, where each individual element
7 identified by a respective matrix notation $X_{i...N}$, wherein the subscript of the matrix
8 notation defines the dimensional indices of the array;

9 taking N aliquots from each sample of each of the multiplicity of biological
10 fluid donations, the number of aliquots taken from each sample defined by the number
11 of dimensional indices comprising the array;

12 forming subpools from the aliquots of each sample, each subpool
13 comprising an aliquot from all of the samples identified by a matrix notation in which
14 one dimensional index is fixed;

15 providing the subpools to a PCR testing facility, wherein all of the
16 subpools are tested for viral indication in a first PCR analysis cycle; and

17 evaluating the dimensional indicia of each subpool which returned a viral
18 positive indication in the first PCR analysis cycle, in accordance with a reduction by
19 the method of minors, the evaluation identifying a unique element defined by the
20 dimensional indicia of each positive subpool if only a single subpool representing each
21 dimensional index returns a positive viral indication, thus unambiguously identifying
22 a viral positive sample. --

Application No. Not yet known

11 10
1 -- 19. The method according to claim 18, wherein the matrix is constructed as
2 a regular, 3-dimensional array, the array further subdivided into rows, columns, and
3 layers, and wherein each element is characterized by a matrix notation X_{rcs} , where the
4 dimensional indices r, c, and s, respectively, identify elements comprising a row, a
5 column, and a layer of the array. --

1 -- 20. The method according to claim 19, wherein the dimensional indicia
2 evaluation identifies a multiplicity of elements defined by the dimensional indicia of
3 each positive subpool, if more than one subpool of a single dimensional index returns
4 a positive viral indication while only a single subpool representing each of the
5 remaining dimensional indices returns a positive viral indication, thus unambiguously
6 identifying more than one unique viral positive samples. --

-- 21. The method according to claim 20, wherein the dimensional indicia evaluation identifies z^n power viral positive candidate elements if multiple subpools representing each dimensional index return a positive viral indication, where z represents the actual number of viral positive samples and where n represents the number of dimensions having multiple positive subpools. --

-- 22. The method according to claim 21, further comprising the step of taking an additional aliquot from each sample identified to each of the z^n viral positive candidate elements:

providing the aliquots to a PCR testing facility, wherein all of the aliquots are tested for viral indication in a second PCR analysis cycle; and
unambiguously identifying all viral positive samples. --

Application No. Not yet known

1 -- 23. The method according to claim 15, wherein the subpool formation step
2 further comprises:

3 forming subpools of aliquots from samples identified by identical r indices
4 but different c and s indices;

5 forming subpools of aliquots from samples identified by identical c indices
6 but different r and s indices;

7 forming subpools of aliquots from samples identified by identical s indices
8 but different r and c indices; and

9 evaluating each of the r, c, and s subpools for a viral positive indication
10 returned by PCR testing. --

1 -- 24. The method according to claim 23, further comprising the steps of:

2 determining the integer index of each r subpool which returned a positive
3 viral indication;

4 determining the integer index of each c subpool which returned a positive
5 viral indication; and

6 determining the integer index of each s subpool which returned a positive
7 viral indication. --

1 -- 25. The method according to claim 24, further comprising the step of
2 substituting the integer indices of each r, c, and s subpool which returned a positive
3 viral indication for the dimensional indices r, c, and s of the matrix notation, thereby
4 identifying a unique matrix element defined by said matrix notation, thus uniquely
5 identifying the corresponding viral positive sample. --

1 -- 26. The method according to claim 25, wherein the 3-dimensional array
2 comprises an 8 x 8 x 8 regular array, the dimensional indices r, c, and s each taking on
3 integer values from 1 to 8. --